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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:28:11 ; Search time 2004.5 Seconds  
(without alignments)  
1964.002 Million cell updates/sec

Title: US-09-636-259C-1  
Perfect score: 1350  
Sequence: 1 atgggtccctgcagccgga.....gggacaggaagcggtatcgtg 1350

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
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39: em\_htgo\_hum:\*  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	1350	100.0	1941	9	AF262016	AF262016 Homo sapi
4	1350	100.0	3612	9	AY032736	AY032736 Homo sapi
5	1350	100.0	3653	9	AF284095	AF284095 Homo sapi
6	1350	100.0	204908	9	AL158163	AL158163 Human DNA
7	1348.4	99.9	1350	6	AX350513	AX350513 Sequence
8	1348.4	99.9	1353	9	AF316894	AF316894 Homo sapi
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13	1106.8	82.0	1552	10	RRU79031	U79031 Rattus norv
14	1095.6	81.2	1380	10	RATRG20	M62372 Rat alpha-2
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16	1084.4	80.3	1454	10	MUSALP2ADB	M99377 Mouse alpha
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ALIGNMENTS

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DEFINITION Sequence 24 from Patent WO0179561.  
ACCESSION AX350512  
VERSION AX350512.1 GI:18616107  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Liggett,S.B. and Small,K.M.  
TITLE Alpha-2 adrenergic receptor polymorphisms  
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;



FEATURES  
source  
Liggett, Stephen B. (US) ; Small, Kersten M. (US)  
Location/Qualifiers  
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/organism="Homo sapiens"  
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Best Local Similarity 100.0%; Pred. No. 2.3e-159;  
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LOCUS Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.  
DEFINITION AF281308 1353 bp DNA linear PRI 05-DEC-2000  
ACCESSION AF281308  
VERSION AF281308.1 GI:9652209  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1353)  
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.  
TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling  
JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)  
MEDLINE 20556293  
PUBMED 10948191  
REFERENCE 2 (bases 1 to 1353)  
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.  
TITLE Direct Submission  
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA  
FEATURES  
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VERSION AF262016.2 GI:9864781  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 1941)  
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,  
Beschi,M. and Agabiti Rosei,E.  
TITLE A search for genetic variability in the human alpha-2 adrenergic  
receptor on chromosome 10  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1941)  
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,  
Beschi,M. and Agabiti Rosei,E.  
TITLE Direct Submission  
JOURNAL Submitted (29-APR-2000) Medical and Surgical Sciences, University  
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy  
REFERENCE 3 (bases 1 to 1941)  
AUTHORS Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,  
Beschi,M. and Agabiti Rosei,E.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-2000) Medical and Surgical Sciences, University  
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy  
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COMMENT On Aug 22, 2000 this sequence version replaced gi:9837145.  
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LOCUS Human alpha 2 adrenergic receptor gene, complete cds.

DEFINITION Human alpha 2 adrenergic receptor gene, complete cds.  
ACCESSION M23533.1  
VERSION M23533.1 GI:178195  
KEYWORDS adrenergic receptor; alpha-2 adrenergic receptor.  
SOURCE Human DNA.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 3604)

REFERENCE

1 Fraser, C.M., Arakawa, S., McCombie, W.R. and Venter, J.C.  
Cloning, sequence analysis, and permanent expression of a human  
alpha 2-adrenergic receptor in Chinese hamster ovary cells.  
Evidence for independent pathways of receptor coupling to adenylate  
cyclase attenuation and activation

AUTHORS

J. Biol. Chem. 264 (20), 11754-11761 (1989)  
89308571  
2568356

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

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GenCore version 5.1.3  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
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- 18: em\_in.\*
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- 21: em\_or.\*
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- 38: em\_sy.\*
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- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
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2	1350	100.0	1353	9	AF316894	AF316894 Homo sapi
3	1348.4	99.9	1350	6	AX350512	AX350512 Sequence
4	1348.4	99.9	1353	9	AF281308	AF281308 Homo sapi
5	1348.4	99.9	1941	9	AF262016	AF262016 Homo sapi
6	1348.4	99.9	3612	9	AY032736	AY032736 Homo sapi
7	1348.4	99.9	3653	9	AF284095	AF284095 Homo sapi
8	1348.4	99.9	204908	9	AL158163	AL158163 Human DNA
9	1325.4	98.2	3604	9	HUMADRA2R	M23533 Human alpha
10	1317.4	97.6	1521	9	HUMADRA	M18415 Human plate
11	1150	85.2	1728	4	PIGA2AR	J05652 Porcine alp
12	1133.8	84.0	2291	10	CPU25722	U25722 Cavia porce
13	1105.2	81.9	1552	10	RRU79031	U79031 Rattus norv
14	1094	81.0	1380	10	RATRG20	M62372 Rat alpha-2
15	1093.4	81.0	2923	4	BTU79030	U79030 Bos taurus
16	1082.8	80.2	1454	10	MUSALP2ADB	M99377 Mouse alpha
17	1082.8	80.2	204317	2	AC113491	AC113491 Mus muscu
18	915.4	67.8	7353	6	AX344975	AX344975 Sequence
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34	463.6	34.3	1380	10	RATRG10	M62371 Rat alpha-2
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36	462	34.2	5221	10	MUSADRA	M97516 Mus musculu
37	460.4	34.1	1704	10	RATA2BADR	M58316 Rat alpha-2
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ALIGNMENTS

RESULT 1	AX350513	AX350513	Sequence 25 from Patent WO0179561.	DNA	linear	PAT 06-FEB-2002
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DEFINITION	AX350513	Sequence 25 from Patent WO0179561.				
ACCESSION	AX350513	Sequence 25 from Patent WO0179561.				
VERSION	AX350513.1	GI:18616108				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Liggett,S.B. and Small,K.M.					
TITLE	Alpha-2 adrenergic receptor polymorphisms					
JOURNAL	Patent: WO 0179561-A 25 25-OCT-2001;					



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DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete  
cds.  
ACCESSION AF281308  
VERSION AF281308.1 GI:9652209  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1353)  
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.  
TITLE An asn to lys polymorphism in the third intracellular loop of the  
human alpha 2A-adrenergic receptor imparts enhanced  
agonist-promoted Gi coupling  
J. Biol. Chem. 275 (49), 38518-38523 (2000)  
JOURNAL 20556293  
MEDLINE 10948191  
REFERENCE 2 (bases 1 to 1353)  
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.  
TITLE Direct Submission  
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of  
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA

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DEFINITION	Homo sapiens adrenergic receptor alpha-2A gene, complete cds.		
ACCESSION	AF262016		
VERSION	AF262016.2	GI:9864781	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1941)		
JOURNAL	Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,		
REFERENCE	Beschi,M. and Agabiti Rosei,E.		
AUTHORS	A search for genetic variability in the human alpha-2 adrenergic		
TITLE	receptor on chromosome 10		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1941)		
AUTHORS	Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,		
TITLE	Beschi,M. and Agabiti Rosei,E.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (29-APR-2000) Medical and Surgical Sciences, University		
AUTHORS	of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy		
TITLE	3 (bases 1 to 1941)		
JOURNAL	Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,		
REFERENCE	Beschi,M. and Agabiti Rosei,E.		
AUTHORS	Direct Submission		
TITLE	Submitted (22-AUG-2000) Medical and Surgical Sciences, University		
JOURNAL	of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy		
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of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACE3.6

This sequence is the entire insert of clone RP11-348N5 The true  
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ACCESSION M23533.1 GI:178195  
VERSION M23533.1  
KEYWORDS adrenergic receptor; alpha-2 adrenergic receptor.  
SOURCE Human DNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3604)  
AUTHORS Fraser,C.M., Arakawa,S., McComble,W.R. and Venter,J.C.  
TITLE Cloning, Sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.  
Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation  
J. Biol. Chem. 264 (20), 11754-11761 (1989)  
MEDLINE 89308571  
PUBMED 2568356  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by W.R.McComble, 30-MAR-1989.  
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QY	61	GGCGGCGCCGGGCCACCCCTTACTCCCTGCAGGTGACGCTGACGCTGGTGTGCCCTGGCC	120		
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Db	2738	CAGATCGCCAAGCGTCGCAACCGCGTGGCCACCCAGCCCGGGGTCCGGACGCCGTCCG	2797		



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:30:36 ; Search time 725.473 Seconds  
(without alignments)  
915.286 Million cell updates/sec

Title: US-09-636-259C-1\_COPY\_730\_770  
Perfect score: 41  
Sequence: 1 gggggcaccgagcgaggcc.....aacggtctggggcccgagcg 41

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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				8:	em_htc:*		
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				#			
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C 1	41	100.0	453	14	BQ129312	BQ129312 ij34d05.y	
C 2	41	100.0	492	14	BM967243	BM967243 ij32c09.y	
C 3	41	100.0	561	14	BM967248	BM967248 ij32d04.y	
4	25	61.0	235	9	AV250353	AV250353 AV250353	
5	25	61.0	3689	11	AK014589	AK014589 Mus muscu	
C 6	24.2	59.0	1350	14	BQ717347	BQ717347 AGENCOURT	

7	24	58.5	763	12	BE905292	BE905292 601499149
C 8	23.6	57.6	434	9	AI189117	AI189117 qc98f10.x
9	23.6	57.6	606	9	AI935256	AI935256 wp16a07.x
C 10	23.6	57.6	925	12	BG172901	BG172901 602337361
C 11	23.4	57.1	463	14	BM800068	BM800068 AGENCOURT
C 12	23.4	57.1	529	14	BM704323	BM704323 UI-E-CK1-
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14	23.4	57.1	659	13	BI330755	BI330755 602982420
C 15	23.4	57.1	793	13	BI952735	BI952735 HVSME000
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18	23	56.1	408	12	BE752287	BE752287 204634 MA
19	23	56.1	420	12	BF600411	BF600411 265187 MA
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21	23	56.1	451	12	BE753851	BE753851 207031 MA
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C 27	23	56.1	737	12	BF315323	BF315323 601902602
C 28	23	56.1	846	12	BG036904	BG036904 602286852
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C 35	23	56.1	1068	13	BI198127	BI198127 602762419
C 36	23	56.1	1568	14	BQ222060	BQ222060 AGENCOURT
C 37	23	56.1	2101	11	AY106418	AY106418 Zea mays
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C 40	22.6	55.1	333	17	B71333	B71333 RPC111-7J9.
41	22.6	55.1	393	13	BI589545	BI589545 RH02982.5
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ALIGNMENTS

RESULT 1	BQ129312/c	BQ129312	453 bp	mRNA	linear	EST 29-APR-2002
LOCUS	ij34d05.y1	Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens				
DEFINITION	CDNA clone IMAGE:6136736 5' similar to SW:A2AA_HUMAN P08913	ALPHA-2A ADRENERGIC RECEPTOR ;				
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ACCESSION	BQ129312	BQ129312				
VERSION	BQ129312.1	GI:20203223				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 453)					
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.					
	Endocrine Pancreas Consortium					
TITLE	Unpublished (2000)					
JOURNAL	Other ESTs: ij34d05.x1					
COMMENT	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue					
	Endocrine Pancreas Consortium					
	Harvard University, Howard Hughes Medical Institute					
	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138					
	Tel: 617-495-1812					

Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center This clone is  
available royalty-free through LNL; please contact the IMAGE  
consortium (info@image.llnl.gov) for further information  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40RP from Gibco.

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made by oligo-dT priming. Size-selected by column  
fractionation; average insert size 1.08 kb. Library was  
amplified once on solid support and plasmid DNA from  
library was prepared. The library DNA was normalized by  
method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
Research 6:791-806; 0.5 microgram single-stranded library  
plasmid DNA was mixed with 5 micrograms PCR product  
representing library inserts and hybridized to an Ecot of  
20. Single-stranded (unhybridized) plasmids were isolated  
by hydroxyapatite chromatography and used to make this  
library."

BASE COUNT 41 a 189 c 164 g 59 t  
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ACCESSION BM967243  
VERSION BM967243.1 GI:19561038  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 492)  
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
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M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,  
Jackson,Y. and Bowers,Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Other\_ESTs: i32c09.x1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812

Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Juliana Brown  
(brown@fas.harvard.edu)  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40RP from Gibco  
High quality sequence stop: 455.

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Site 2: Sal 1; Starting library constructed using  
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made by oligo-dT priming. Size-selected by column  
fractionation; average insert size 1.08 kb. Library was  
amplified once on solid support and plasmid DNA from  
library was prepared. The library DNA was normalized by  
method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
Research 6:791-806; 0.5 microgram single-stranded library  
plasmid DNA was mixed with 5 micrograms PCR product  
representing library inserts and hybridized to an Ecot of  
20. Single-stranded (unhybridized) plasmids were isolated  
by hydroxyapatite chromatography and used to make this  
library."

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Query Match 100.0%; Score 41; DB 14; Length 492;  
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Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGCACCGAGCGCAGGCCAACGGTCTGGGCCCCGAGCG 41  
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Db 441 GGGGCACCGAGCGCAGGCCAACGGTCTGGGCCCCGAGCG 401

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cDNA clone IMAGE:6136374 5' similar to SW:A2AA\_HUMAN P08913  
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.  
ACCESSION BM967248  
VERSION BM967248.1 GI:19561047  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 561)  
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas  
M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,  
Jackson,Y. and Bowers,Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Other\_ESTs: i32d04.x1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138

Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Juliana Brown  
(brown@fas.harvard.edu)  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40RP from Gibco  
High quality sequence stop: 445.

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/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;  
Site 2: Sal 1; Starting library constructed using  
SuperScript Plasmid Library kit (Life Technologies). cDNA  
made by oligo-dT priming. Size-selected by column  
fractionation; average insert size 1.08 kb. Library was  
amplified once on solid support and plasmid DNA from  
library was prepared. The library DNA was normalized by  
method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
Research 6:791-806; 0.5 microgram single-stranded library  
plasmid DNA was mixed with 5 micrograms PCR product  
representing library inserts and hybridized to an Ecot of  
20. Single-stranded (unhybridized) plasmids were isolated  
by hydroxyapatite chromatography and used to make this  
library."

BASE COUNT 63 a 215 c 210 g 73 t  
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Query Match 100.0%; Score 41; DB 14; Length 561;  
Best Local Similarity 100.0%; Pred. No. 0.00057;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGCCCAACGGTCTGGGCCCCGAGCG 41  
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RESULT 4  
AV250353 235 bp mRNA linear EST 04-NOV-1999  
LOCUS  
DEFINITION  
AV250353 RIKEN full-length enriched, 0 day neonate head Mus  
musculus cDNA clone 4833422I09 3', mRNA sequence.  
ACCESSION  
AV250353 GI:6237812  
VERSION  
KEYWORDS  
EST.  
SOURCE  
house mouse.

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 235)  
AUTHORS  
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,  
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,  
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai  
C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,  
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata  
Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,  
Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y.,  
Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,  
Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al. 1999)

TITLE  
JOURNAL  
COMMENT  
Unpublished (1999)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic

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The Institute of Physical and Chemical Research (RIKEN)  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/  
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,  
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki  
Y.

Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for  
further details.

FEATURES  
source

Location/Qualifiers  
1. .235  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="4833422I09"  
/clone\_lib="RIKEN full-length enriched, 0 day neonate  
head"  
/sex="mixed"  
/tissue\_type="head"  
/dev\_stage="0 day neonate"  
/lab\_host="DH10B"  
/note="Site 1: Sall; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 10.0 and subtraction to Rot = 100.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGAGATTCTCGAGTTAATAATTAATCCCCCCCCCCC  
3']. cDNA was cloned into the XhoI and BamHI sites.  
Vector: a modified pBluescript KS(+) after bulk excision  
from Lambda FLC I."

BASE COUNT 52 a 58 c 66 g 59 t  
ORIGIN

Query Match 61.0%; Score 25; DB 9; Length 235;  
Best Local Similarity 75.6%; Pred. No. 1.1e+02;  
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGCGCCCAACGGTCTGGGCCCCGAGCG 41  
|||||  
Db 94 GGGGGCACCAGCGCGCCCAATGGTGTGGTCTGGAGCG 134

RESULT 5  
AK014589  
LOCUS

DEFINITION  
AK014589 3689 bp mRNA linear HTC 19-JAN-2002  
Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched  
library, clone:4632419J12.homolog to ALPHA-1-ANTIPROTEINASE  
PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR),  
full insert sequence.

ACCESSION  
VERSION  
KEYWORDS  
AK014589  
AK014589.1 GI:12852536  
HTC; CAP trapper.

SOURCE Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA, clone\_lib:RIKEN full-length enriched mouse cDNA library clone:4632419J12.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5 (bases 1 to 3689)

AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishii,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAGAAGGATCCCAAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised between 3 and 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI. Host: DH10B.

FEATURES

Location/Qualifiers

1. .3689

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="FANTOM\_DB:4632419J12"

/db\_xref="MGD:MGI:1899072"

/db\_xref="taxon:10090"

/clone="4632419J12"

/tissue type="skin"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="0 day neonate"

199. .1440

/note="data source:SPTR, source key:P17475, evidence:ISS homolog to ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) putative"

/codon\_start=1

/protein\_id="BAB29447.1"

/db\_xref="GI:12852537"

/db\_xref="MGD:MGI:1915304"

/translation="MTRMLDLGLFLAGLLTVKGLLQDRDAPDMDSPVRVQEWRGKKDARQLARHNMEFGFKLLQRLASNSPQGNIFLSPLSISAFSMLSLGAQNSTLEEIREGF NFKEMSNWDVHAAPHYLLHKLNQETEDTKMNLGNALFMDQKLRPQORFLNAKNVYDADMLVTNFDLENTQKDINRIVISQKTHSRKKNMVKSIDPGTVMILTNYIYFRGRWQYEFDPKQTKEEFFIEKGTKVKPMMFQRLYDMAYDSQLSCTILEIPYRGNITATFVLDPD NGKLLLEQGLQADIFAKWKSLLSKRVVDVWVPKLRISSTYNMKKVL SRLGSKIPEE NGDLTRISSHRSRLKVGAEAVHKAELKMDEKMEGAGSQAOTLPMETPRHMKLDRPFLM MIYENFMPSMVFLARIYDPSG"

polyA\_signal 3670. .3675

/note="putative"

3689

/note="putative"

BASE COUNT 966 a 955 c 910 g 857 t 1 others

ORIGIN

Query Match 61.0%; Score 25; DB 11; Length 3689;

Best Local Similarity 75.6%; Pred. No. 1.8e+02;

Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCGAGGCCCAACGGTCTGGGCCCGGAGCG 41

|||||

Db 2249 GGGGGCACCAAGGGCCAGACCAATGGTGTGGTCTGGAGCG 2289

|||||

RESULT 6

BQ717347/c 1350 bp mRNA linear EST 16-JUL-2002

LOCUS

DEFINITION AGENCOURT\_8486512 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone





Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM12212 row: c column: 05  
High quality sequence stop: 462.  
Location/Qualifiers  
1. .463  
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/db\_xref="taxon:9606"  
/clone="IMAGE:5531068"  
/clone\_lib="NIH\_MGC\_71"  
/tissue\_type="leiomyosarcoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.1 kb. "  
90 a 160 c 130 g 83 t

FEATURES  
source

BASE COUNT 90 a 160 c 130 g 83 t  
ORIGIN  
  
Query Match 57.1%; Score 23.4; DB 14; Length 463;  
Best Local Similarity 73.2%; Pred. No. 4.3e+02;  
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCACCGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41  
|||||  
Db 358 GGGGGCACCGCGCAGGGACGGCGGCTTGGGCGCAGAGG 318  
  
RESULT 12  
BM704323/c  
LOCUS 529 bp mRNA linear EST 28-FEB-2002  
DEFINITION UI-E-CK1-afj-j-22-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone  
UI-E-CK1-afj-j-22-0-UI 5', mRNA sequence.  
BM704323  
ACCESSION BM704323.1 GI:19017581  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 529)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1. .529  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-CK1-afj-j-22-0-UI"  
/clone\_lib="UI-E-CK1"  
/tissue\_type="Retina Foveal and Macular"  
/dev\_stage="adult"

FEATURES  
source

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-CK1 is a normalized CDNA library containing the  
following tissue(s): Retina Foveal and Macular. The  
library was constructed according to Bonaldo, Lennon and  
Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into pT7T3-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dT)18 tail. The sequence tag for this  
library is GTCC. This library was created for the program,  
Gene Discovery in the Visual System, supported by National  
Eye Institute (NEI)."  
83 a 173 c 161 g 111 t 1 others  
ORIGIN  
  
Query Match 57.1%; Score 23.4; DB 14; Length 529;  
Best Local Similarity 73.2%; Pred. No. 4.4e+02;  
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCACCGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41  
|||||  
Db 288 GGGGGCACCGCGCAGGGACGGCGGCTTGGGCGCAGAGG 248  
  
RESULT 13  
BM671529  
LOCUS 606 bp mRNA linear EST 27-FEB-2002  
DEFINITION UI-E-CK1-afj-j-22-0-UI.s2 UI-E-CK1 Homo sapiens cDNA clone  
UI-E-CK1-afj-j-22-0-UI 3', mRNA sequence.  
BM671529  
ACCESSION BM671529.1 GI:18981427  
VERSION  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 606)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 Forward  
POLYA=Yes.  
Location/Qualifiers  
1. .606  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-CK1-afj-j-22-0-UI"  
/clone\_lib="UI-E-CK1"  
/tissue\_type="Retina Foveal and Macular"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

FEATURES  
source

UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG\_LIB=UI-E-CK1  
TAG\_TISSUE=Foveal and Macular Retina  
TAG\_SEQ=GTCC"

BASE COUNT 138 a 173 c 189 g 104 t 2 others  
ORIGIN

Query Match 57.1%; Score 23.4; DB 14; Length 606;  
Best Local Similarity 73.2%; Pred. No. 4.5e+02;  
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41  
|||||  
Db 325 GGGGGCACCGAGCGCAGGGACGCGGGCCTGGGCGCAGAGG 365  
|||||

RESULT 14  
BI330755 602982420F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:5135261 5',  
LOCUS mRNA sequence.  
DEFINITION BI330755 659 bp mRNA linear EST 30-JUL-2001  
ACCESSION BI330755.1 GI:15015412  
VERSION  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE 1 (bases 1 to 659)  
JOURNAL NIH-MGC <http://mgc.nci.nih.gov/>.  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM11332 row: 9 column: 06  
High quality sequence stop: 655.  
Location/Qualifiers  
1. .659

FEATURES  
source  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5135261"  
/clone\_lib="NCI\_CGAP\_Li9"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 148 a 153 C 191 g 167 t  
ORIGIN

Query Match 57.1%; Score 23.4; DB 13; Length 659;  
Best Local Similarity 73.2%; Pred. No. 4.6e+02;

Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCACCGAGCGCAGGCCCAACGGTCTGGGCCCCGAGCG 41  
|||||  
Db 387 GGGGGCACTAAGGCCAGGCCCAATGGTGTGGGTCTGGAGCG 427  
|||||

RESULT 15  
BI952735/c 793 bp mRNA linear EST 19-OCT-2001  
LOCUS HVSMEm0007J12f Hordeum vulgare green seedling EST library  
DEFINITION HVCDNA0014 (Blumeria infected) Hordeum vulgare cDNA clone  
HVSMEm0007J12f, mRNA sequence.  
ACCESSION BI952735  
VERSION BI952735.1 GI:16296792  
KEYWORDS EST.  
SOURCE Hordeum vulgare.  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,  
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons  
,J., Oates,R. and Main,D.  
TITLE Development of a genetically and physically anchored EST resource  
for barley genomics: Blumeria infected Morex (compatible) seedling  
cDNA library  
JOURNAL Unpublished (2001)  
COMMENT Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: [rwing@clemson.edu](mailto:rwing@clemson.edu)  
Total hg bases = 198  
Seq primer: AATTAAACCTCACTAAAGGG  
High quality sequence start: 22  
High quality sequence stop: 590.  
Location/Qualifiers  
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/db\_xref="taxon:4513"  
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HVCDNA0014 (Blumeria infected)"  
/tissue\_type="green seedling leaf"  
/lab\_host="TJC121"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Morex (mla) plants were greenhouse grown in the R  
Wise lab at Iowa State University, Ames, IA; 7 day old  
green seedlings were infected with isolate 5874 of  
Blumeria graminis f. sp. hordei, and leaves were harvested  
24, 48 and 72 hr post-inoculation and snap frozen (Wise).  
In the TJ Close lab at the University of California,  
Riverside, total RNA was prepared from each sample pool,  
equal quantities of all three RNA pools were combined,  
poly(A) RNA was purified from the mixture, one primary  
unamplified cDNA library was made, and 1 million pfu were  
in vivo excised to give pBluescript SK(-) cDNA phagemids  
(Chin). Phagemids were plated and picked at the Clemson  
University Genomics Institute (CUGI) (Begum, Palmer,  
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
sequencing and sequence analysis were performed at CUGI  
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
The sequence has been trimmed to remove vector sequence  
and contains a minimum of 100 bases of phred value 20 or  
above. For more details on library preparation and  
sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
this clone see <http://www.genome.clemson.edu/orders> Also

see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30.  
(http://wheat.pw.usda.gov/ggpapes/bgn/31/cover.html)"

BASE COUNT      180 a    240 c    229 g    144 t  
ORIGIN

Query Match                    57.1%;    Score 23.4;    DB 13;    Length 793;  
Best Local Similarity    73.2%;    Pred. No. 4.7e+02;  
Matches    30;    Conservative    0;    Mismatches    11;    Indels    0;    Gaps    0;

QY    1    GGGGGCACCGAGCGCGAGCCCAACGGTCTGGGCCCCCGAGCG    41  
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Db    743    GGGGGTTCCGCCCCCGCCAGCCTAAGGTTCTGGGCCCCCGAGTG    703

Search completed: March 11, 2003, 07:38:58  
Job time : 733.473 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: March 10, 2003, 18:28:11 ; Search time 20004.5 Seconds  
(without alignments)  
1964.002 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_htg:\*  
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4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
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16: em\_fun:\*  
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18: em\_in:\*  
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41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1350	100.0	1941	9	AF262016	AF262016 Homo sapi
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5	1350	100.0	3653	9	AF284095	AF284095 Homo sapi
6	1350	100.0	204908	9	AL158163	AL158163 Human DNA
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10	1319	97.7	1521	9	HUMADRA	M18415 Human plate
11	1150	85.2	1728	4	PIGA2AR	J05652 Porcine alp
12	1133.8	84.0	2291	10	CPU25722	U25722 Cavia porce
13	1106.8	82.0	1552	10	RRU79031	U79031 Rattus norv
14	1095.6	81.2	1380	10	RATRG20	M62372 Rat alpha-2
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37	458.8	34.0	1704	10	RATA2BADR	M58316 Rat alpha-2
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ALIGNMENTS

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ACCESSION AX350512  
VERSION AX350512.1 GI:18616107  
KEYWORDS human.  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Liggett,S.B. and Small,K.M.  
TITLE Alpha-2 adrenergic receptor polymorphisms  
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;

AX350512 Sequence 24 from Patent WO0179561. linear PAT 06-FEB-2002



Liggett, Stephen B. (US) ; Small, Kersten M. (US)

FEATURES

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BASE COUNT 199 a 490 c 441 g 220 t  
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Best Local Similarity 100.0%; Pred. No. 2.3e-159;

Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AF281308

LOCUS

DEFINITION

AF281308.1

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

mRNA

CDS

AF281308 Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.  
1353 bp DNA linear PRI 05-DEC-2000  
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1 (bases 1 to 1353)  
Small K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.  
An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling  
J. Biol. Chem. 275 (49), 38518-38523 (2000)  
20556293  
10948191  
2 (bases 1 to 1353)  
Small, K.M., Forbes, S.L., Bridges, K.M. and Liggett, S.B.  
Direct Submission  
Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA  
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1 (bases 1 to 1941)  
Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,  
Beschi,M. and Agabiti Rosei,E.  
A search for genetic variability in the human alpha-2 adrenergic  
receptor on chromosome 10  
Unpublished  
2 (bases 1 to 1941)  
Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,  
Beschi,M. and Agabiti Rosei,E.  
Direct Submission  
Submitted (29-APR-2000) Medical and Surgical Sciences, University  
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy  
3 (bases 1 to 1941)  
Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,  
Beschi,M. and Agabiti Rosei,E.  
Direct Submission  
Submitted (22-AUG-2000) Medical and Surgical Sciences, University  
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy  
Sequence update by submitter  
On Aug 22, 2000 this sequence version replaced gi:9837145.  
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LOCUS Human platelet alpha-2-adrenergic receptor gene, complete cds.
DEFINITION
ACCESSION M18415
VERSION M18415.1 GI:178191
KEYWORDS alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE Human (lambda-EMBL 3 library) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1521)
AUTHORS Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
MEDLINE 88042789
PUBMED 2823383
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GenCore version 5.1.3  
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9816.632 Million cell updates/sec

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 10: gb\_ro:\*
- 11: gb\_sts:\*
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- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1350	100.0	1353	9	AF316894	AF316894 Homo sapi
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4	1348.4	99.9	1353	9	AF281308	AF281308 Homo sapi
5	1348.4	99.9	1941	9	AF262016	AF262016 Homo sapi
6	1348.4	99.9	3612	9	AY032736	AY032736 Homo sapi
7	1348.4	99.9	3653	9	AF284095	AF284095 Homo sapi
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11	1150	85.2	1728	4	PIGA2AR	J05652 Porcine alp
12	1133.8	84.0	2291	10	CPU25722	U25722 Cavia porce
13	1105.2	81.9	1552	10	RRU79031	U79031 Rattus norv
14	1094	81.0	1380	10	RATRG20	M62372 Rat alpha-2
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16	1082.8	80.2	1454	10	MUSALP2ADB	M99377 Mouse alpha
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Liggett,S.B. and Small,K.M.					
TITLE	Alpha-2 adrenergic receptor polymorphisms					
JOURNAL	Patent: WO 0179561-A 25 25-OCT-2001;					



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LOCUS Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.  
DEFINITION Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.

ACCESSION AF281308

VERSION AF281308.1 GI:9652209

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1353)

AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.

TITLE An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling

JOURNAL J. Biol. Chem. 275 (49), 38518-38523 (2000)

MEDLINE 20556293

PUBMED 10948191

REFERENCE 2 (bases 1 to 1353)

AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.

TITLE Direct Submission

JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA

FEATURES

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AF262016  
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DEFINITION Homo sapiens adrenergic receptor alpha-2A gene, complete cds.  
ACCESSION AF262016  
VERSION AF262016.2 GI:9864781  
1941 bp DNA linear PRI 22-AUG-2000

KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1941) Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Beschi, M. and Agabiti Rosei, E.
TITLE	A search for genetic variability in the human alpha-2 adrenergic receptor on chromosome 10
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1941)
AUTHORS	Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, C., Beschi, M. and Agabiti Rosei, E.

TITLE	Direct Submission
JOURNAL	Submitted (29-APR-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REFERENCE	3 (bases 1 to 1941)
AUTHORS	Castellano,M., Glacche',M., Rossi,F., Rivadossi,F., Perani,C., Beschi,M. and Agabiti Rosei,E.
TITLE	Direct Submission
JOURNAL	Submitted (22-AUG-2000) Medical and Surgical Sciences, University of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
REMARK	Sequence update by submitter
COMMENT	On Aug 22, 2000 this sequence version replaced gi:9837145.
FEATURES	

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153

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RESULT 10
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LOCUS      Human platelet alpha-2-adrenergic receptor gene, complete cds.
DEFINITION      1521 bp      DNA
ACCESSION      M18415
VERSION      M18415.1 GI:178191
KEYWORDS      alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE      Human (lambda-EMBL 3 library) DNA.
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 1521)
AUTHORS      Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
      Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
TITLE      Cloning, sequencing, and expression of the gene coding for the
      human platelet alpha 2-adrenergic receptor
JOURNAL      Science 238 (4827), 650-656 (1987)
MEDLINE      88042789
PUBMED      2823383
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